Full wwPDB NMR Structure Validation Report (i)

Feb 22, 2022 – 11:11 AM EST

PDB ID	:	1VEX
Title	:	F-spondin TSR domain 4
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Deposited on	:	2004-04-06

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

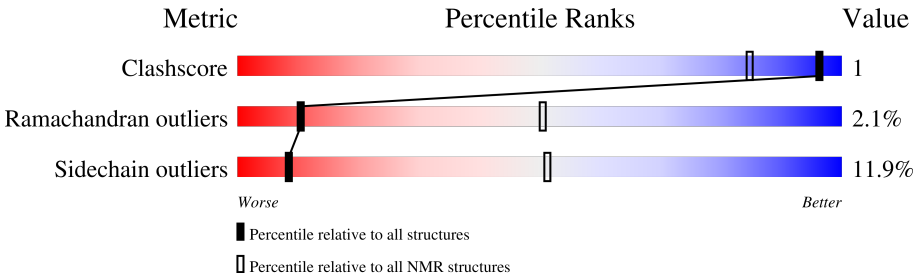
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	56	91% · 5%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 14 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:614-A:666 (53)	0.67	14

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters. No single-model clusters were found.

Cluster number	Models
1	2, 3, 4, 6, 7, 8, 9, 12, 13, 14, 15, 16, 18, 20
2	5, 10, 17, 19
3	1, 11

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 837 atoms, of which 410 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called F-spondin.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	56	837	260	410	73	85	9	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	611	GLY	-	cloning artifact	UNP P35446
A	612	SER	-	cloning artifact	UNP P35446

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: F-spondin

Chain A: 

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

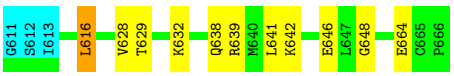
• Molecule 1: F-spondin

Chain A: 

4.2.2 Score per residue for model 2

• Molecule 1: F-spondin

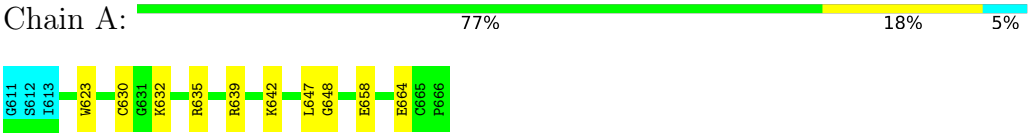
Chain A: 



4.2.3 Score per residue for model 3

• Molecule 1: F-spondin

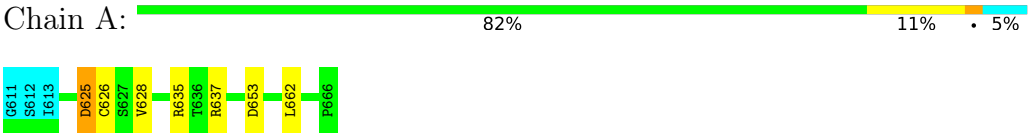
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: F-spondin

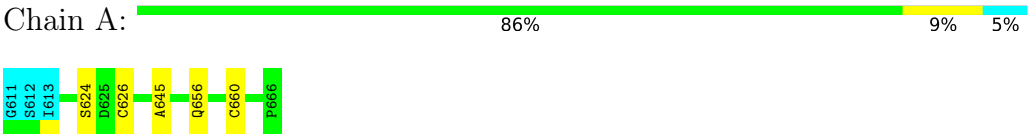
Chain A:



4.2.5 Score per residue for model 5

• Molecule 1: F-spondin

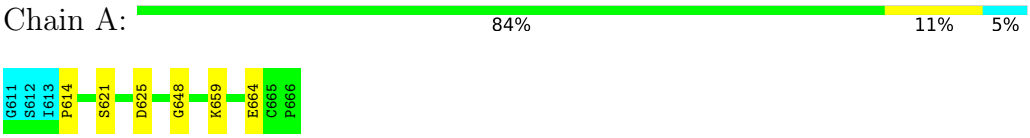
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: F-spondin

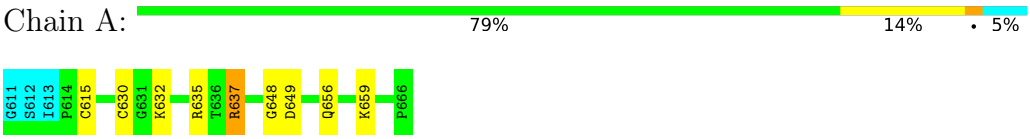
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: F-spondin

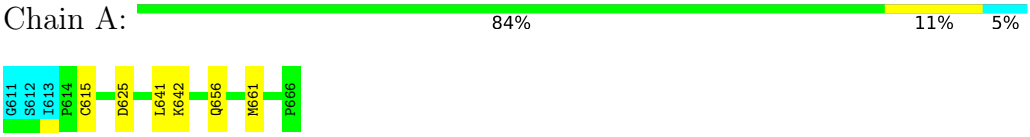
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: F-spondin

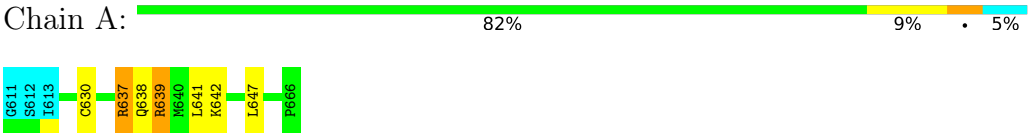
Chain A:



4.2.9 Score per residue for model 9

• Molecule 1: F-spondin

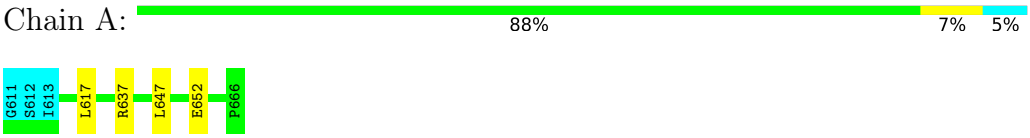
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: F-spondin

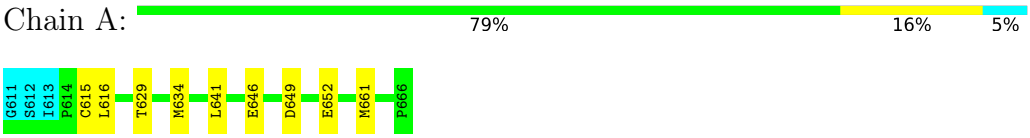
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: F-spondin

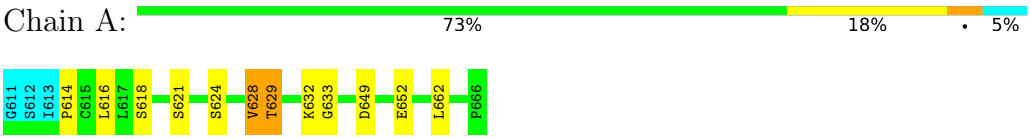
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: F-spondin

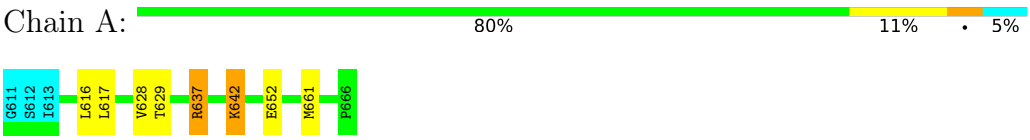
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: F-spondin

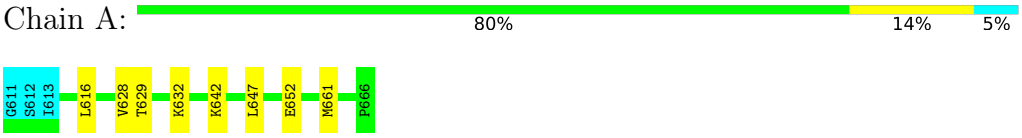
Chain A:



4.2.14 Score per residue for model 14 (medoid)

• Molecule 1: F-spondin

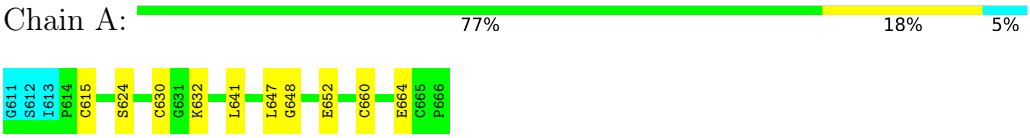
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: F-spondin

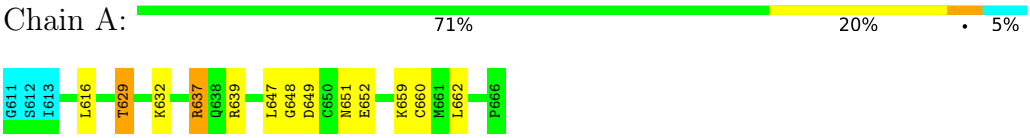
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: F-spondin

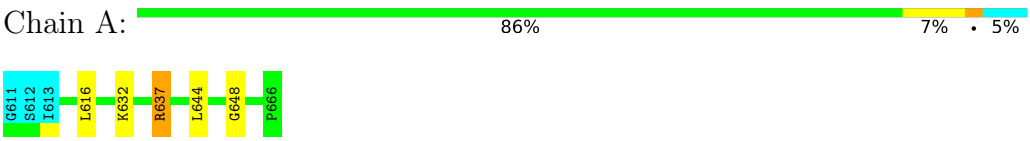
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: F-spondin

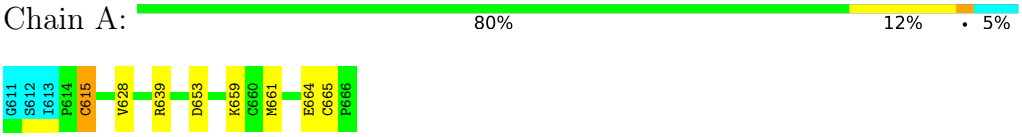
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: F-spondin

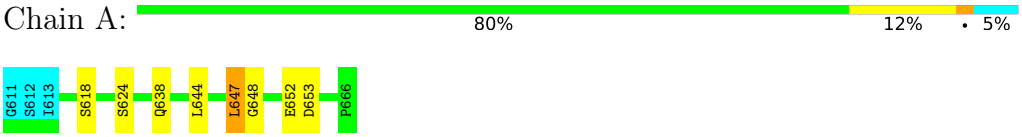
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: F-spondin

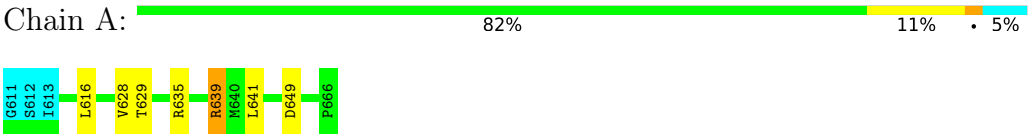
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: F-spondin

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.0.30
OPALp	refinement	1.3

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.50±0.01	0±0/416 (0.0± 0.0%)	1.09±0.05	1±1/559 (0.1± 0.2%)
All	All	0.51	0/8320 (0.0%)	1.09	16/11180 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.3±0.6
All	All	0	7

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	637	ARG	NE-CZ-NH1	9.20	124.90	120.30	13	4
1	A	637	ARG	CD-NE-CZ	7.93	134.71	123.60	13	3
1	A	639	ARG	NE-CZ-NH2	-7.39	116.60	120.30	18	5
1	A	635	ARG	NE-CZ-NH2	-6.32	117.14	120.30	3	1
1	A	628	VAL	CA-CB-CG2	6.17	120.15	110.90	12	1
1	A	637	ARG	NE-CZ-NH2	-5.96	117.32	120.30	17	1
1	A	639	ARG	NE-CZ-NH1	5.09	122.85	120.30	9	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	635	ARG	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	637	ARG	Sidechain	3
1	A	639	ARG	Sidechain	1

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	409	391	391	1±1
All	All	8180	7820	7820	12

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:644:LEU:H	1:A:644:LEU:HD23	0.54	1.62	19	1
1:A:647:LEU:HD13	1:A:648:GLY:H	0.53	1.63	19	1
1:A:642:LYS:HE2	1:A:642:LYS:HA	0.51	1.82	13	1
1:A:664:GLU:H	1:A:664:GLU:CD	0.50	2.10	3	1
1:A:629:THR:HA	1:A:662:LEU:HD12	0.49	1.85	12	1
1:A:628:VAL:CG1	1:A:633:GLY:HA3	0.46	2.41	12	1
1:A:623:TRP:CH2	1:A:658:GLU:HB2	0.44	2.46	3	1
1:A:629:THR:HA	1:A:662:LEU:HD23	0.42	1.91	16	1
1:A:617:LEU:HD21	1:A:652:GLU:HG3	0.41	1.93	13	1
1:A:616:LEU:H	1:A:647:LEU:CD2	0.41	2.29	1	1
1:A:625:ASP:CG	1:A:626:CYS:H	0.41	2.19	4	1
1:A:626:CYS:SG	1:A:662:LEU:HD21	0.41	2.56	4	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	52/56 (93%)	46±2 (88±3%)	5±2 (9±4%)	1±1 (2±2%)	10 50
All	All	1040/1120 (93%)	920 (88%)	98 (9%)	22 (2%)	10 50

All 10 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	648	GLY	7
1	A	625	ASP	3
1	A	616	LEU	2
1	A	614	PRO	2
1	A	649	ASP	2
1	A	615	CYS	2
1	A	626	CYS	1
1	A	645	ALA	1
1	A	646	GLU	1
1	A	661	MET	1

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	48/50 (96%)	42±2 (88±5%)	6±2 (12±5%)	8 51
All	All	960/1000 (96%)	846 (88%)	114 (12%)	8 51

All 29 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	632	LYS	9
1	A	616	LEU	8
1	A	628	VAL	7
1	A	629	THR	7
1	A	647	LEU	7
1	A	652	GLU	7
1	A	641	LEU	6
1	A	642	LYS	6

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Mol	Chain	Res	Type	Models (Total)
1	A	624	SER	5
1	A	637	ARG	5
1	A	664	GLU	4
1	A	630	CYS	4
1	A	659	LYS	4
1	A	615	CYS	4
1	A	661	MET	4
1	A	638	GLN	3
1	A	653	ASP	3
1	A	656	GLN	3
1	A	660	CYS	3
1	A	649	ASP	3
1	A	621	SER	2
1	A	639	ARG	2
1	A	618	SER	2
1	A	646	GLU	1
1	A	617	LEU	1
1	A	634	MET	1
1	A	651	ASN	1
1	A	644	LEU	1
1	A	665	CYS	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided